L Number	Hits	Search Text	DB	Time stamp
1	67	cox$.in. and mismatch	USPAT; US-PGPUB	2003/08/26 17:27
2	3	cox$.in. and mismatch.ti.	USPAT; US-PGPUB	2003/08/26 17:28
3	1	mismatch near3 (corepair or co adj1 repair)	USPAT; US-PGPUB	2003/08/26 17:29

```
     (FILE 'HOME' ENTERED AT 17:32:59 ON 26 AUG 2003)

     FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 17:33:06 ON 26 AUG 2003
L1             9 S MISMATCH? (5A) (COREPAIR OR CO(W)REPAIR)
L2             3 DUP REM L1 (6 DUPLICATES REMOVED)

     FILE 'SCISEARCH' ENTERED AT 17:34:00 ON 26 AUG 2003
L3          5411 S CARRAWAY?/RAU
L4          2307 S L3 AND 1993/RPY
L5           180 S L4 AND 175/RVL
L6             0 S L5 AND MULTIPLEX?
L7            16 S L5 AND MULTIPL?

=> d 15 126 bib ab

L5   ANSWER 126 OF 180  SCISEARCH  COPYRIGHT 2003 THOMSON ISI on STN
AN   96:94649  SCISEARCH
GA   The Genuine Article (R) Number: TQ968
TI   A NOVEL IN-VIVO METHOD TO DETECT DNA-SEQUENCE VARIATION
AU   FAHAM M; COX D R (Reprint)
CS   STANFORD UNIV, SCH MED, DEPT GENET & PEDIAT, STANFORD, CA, 94305
     (Reprint); STANFORD UNIV, SCH MED, DEPT GENET & PEDIAT, STANFORD, CA,
     94305; UNIV CALIF SAN FRANCISCO, DEPT BIOCHEM & BIOPHYS, SAN FRANCISCO,
     CA, 94143
CYA  USA
SO   GENOME RESEARCH, (DEC 1995) Vol. 5, No. 5, pp. 474-482.
     ISSN: 1054-9803.
DT   Article; Journal
FS   LIFE
LA   ENGLISH
REC  Reference Count: 27
     *ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*
AB       Mismatch repair detection (MRD) is an in vivo method that uses a change
     in bacterial colony color to detect DNA sequence variation. DNA fragments
     to be screened for variation are cloned into two MRD plasmids, and
     bacteria are transformed with heteroduplexes of these constructs. The
     resulting colonies are blue in the absence of a mismatch and white in the
     presence of a mismatch. MRD is capable of detecting a single mismatch in a
     DNA fragment as large as 10kb in size. In addition, MRD has the potential
     for analyzing many fragments simultaneously, offering a powerful method
     for high-throughput genotyping and mutation detection in a large genomic
     region.


=>
```